



Blast 2 Sequences results

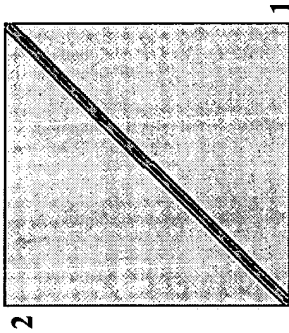
PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: ☒ Filter

Sequence 1 lc|seq_1 Length 8509 (1 .. 8509)

Sequence 2 lc|seq_2 Length 8509 (1 .. 8509)



=====

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 1.626e+04 bits (8455), Expect = 0.0
Identities = 8482/8509 (99%)
Strand = Plus / Plus

=====

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Blast Result

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```

CPU time: 0.07 user secs. 0.02 sys. secs 0.09 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 3000
Number of extensions: 67
Number of successful extensions: 16
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 8509
Length of database: 12,527,565,053
Length adjustment: 28
Effective length of query: 8481
Effective length of database: 12,527,565,025
Effective search space: 106246278977025
Effective search space used: 106246278977025
Neighboring words threshold: 0
Window for multiple hits: 0
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 23 (44.9 bits)